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L40: Entry 1 of 2 File: USPT Oct 29, 2002

DOCUMENT-IDENTIFIER: US 6472154 B1
TITLE: Polymorphic repeats in human genes

Detailed Description Paragraph Table (170):
L26953 3'UTR 4.16 2797 CAAAAA L27560 UNKNOWN 6 3438 GTT L27560 UNKNOWN 14 3658 A L27745 CDS 7 1067 AG L30117 UNKNOWN 79 652 T L31881 3'UTR 4.59 1481 CCCAG L32832 CDS 2.93 2092 GAGGAGGAGGAAGAA (SEQ ID NO:254) L32832 CDS 10 5866 CAA L32832 CDS 7.66 10261 CAG L32832 CDS 7 2985 GGC L33075 3'UTR 16 6723 A L33243 3'UTR 9 13947 TG L33477 3'UTR 10 3557 CA L34357 CDS 6 590 GGC L34408 UNKNOWN 15 706 A L35592 UNKNOWN 14 1577 AC L36140 5'UTR 24 1 T L36642 3'UTR 4 4333 CAAAA L36983 3'UTR 5.66 3368 CTC L37112 CDS 3.5 1257 CCTCAG L37198 UNKNOWN 23 7 A L38707 CDS 3.83 146 CCGGGG L38951 3'UTR 31 3653 A L38951 3'UTR 13 3736 T L38961 3'UTR 22 2283 T L39064 CDS 8.33 1504 AGC L39833 3'UTR 13 1809 A L39833 3'UTR 13 2713 T L40377 5'UTR 6.66 33 GCG L40377 5'UTR 6.33 51 GCA L40392 3'UTR 14 2209 T L40992 CDS 6 18 CAG L40992 BORDER 5.66 0 CAG L41690 CDS 6 620 GCC L41887 3'UTR 14 2046 A L41919 CDS 8 440 GGC L42025 5'UTR 5.66 1 GGC L42243 3'UTR 7 3934 GT L42243 3'UTR 16 2217 T L42243 3'UTR 15 1137 T L42243 3'UTR 12 2874 A L44505 UNKNOWN 13 309 A L46353 5'UTR 2.8 2094 CACACTCACA (SEQ ID NO:255) L46353 5'UTR 19 2401 TC L46353 5'UTR 9.5 2381 TC L46353 5'UTR 6.5 1394 TG L46353 5'UTR 13 264 A L46353 3'UTR 5 3378 TGGGG L48796 UNKNOWN 15 147 A L49169 3'UTR 6 1661 GAG L49169 3'UTR 6.5 2689 CT L49380 CDS 6 1771 GCC L76702 CDS 4.33 301 CAGCCC L76703 3'UTR 12 2219 A L77864 CDS 5.66 571 GAG L78833 3'UTR 18 6465 A M10901 3'UTR 18 3217 A M11220 3'UTR 5.5 693 TATT M11353 3'UTR 16 817 A M11722 5'UTR 14 216 G M12783 UNKNOWN 3.85 296 CGCAGCT M12783 UNKNOWN 7.5 3612 AC M12783 UNKNOWN 16 238 A M13232 3'UTR 6.5 1889 CA M13452 3'UTR 8.5 2030 GA M13452 3'UTR 15 1745 A M13903 CDS 5 528 GAGCAGCAGGAGGGGCAGCTGGAGCTCCCA (SEQ ID NO:256) M13903 CDS 3.43 679 AGCAGCAGGAGGGGCAGCTGGAGCTCTCTG (SEQ ID NO:257) M14058 3'UTR 12 2221 A M14083 3'UTR 7 2667 AT M14170 CDS 7.66 30 TGC M14219 3'UTR 13 1660 T M14630 UNKNOWN 12 538 A M14648 3'UTR 10.66 3535 TTG M14745 3'UTR 7.5 897 AC M14764 5'UTR 3.6 36 AGCGC M14764 3'UTR 7 2444 CA M15169 UNKNOWN 13 2852 C M15353 3'UTR 18 847 T M16276 UNKNOWN 12 1368 A M16505 UNKNOWN 6.5 2611 AC M16505 UNKNOWN 18 3645 A M16801 CDS 3.83 2295 CCCCCA M16937 3'UTR 2.7 865 AAACAAA (SEQ ID NO:258) M16938 5'UTR 7 172 TG M16965 CDS 2.94 115 TACCTTTGTTGGAAGACG (SEQ ID NO:259) M16965 CDS 2.5 591 CTGGAAGACATGGATTTT (SEQ ID NO:260) M18533 UNKNOWN 5.25 12297 TTGA M18533 UNKNOWN 8.5 11725 AC M18728 UNKNOWN 12 2266 A M19154 3'UTR 7.33 2117 ACA M19961 5'UTR 13 0 T M20681 UNKNOWN 13 2233 T M20681 UNKNOWN 13 3705 A M21305 CDS 6.4 56 TGGAA M21305 BORDER 3.8 0 ATGGA M21574 3'UTR 14 4503 T M23114 3'UTR 3.8 3839 CACCC M23263 CDS 20.33 1884 GGC M23263 CDS 17 701 GCA M24069 CDS 7.66 229 CCA M24283 3'UTR 9 2742 GT M24486 3'UTR 16 2350 T M24902 3'UTR 12.5 2338 AATA M25667 3'UTR 9 1153 CT M25667 3'UTR 17 973 A M28170 3'UTR 17 1816 GT M28713 5'UTR 6.66 253 CGG M29053 3'UTR 3.8 1579 AAAAT M29204 UNKNOWN 21 288 A M29873 3'UTR 6.5 1687 TA M29874 3'UTR 7 1688 AT M29874 3'UTR 15 2510 T M30448 3'UTR 26 887 A M31165 BORDER 12 900 A M31523 3'UTR 12 2316 T M31525 3'UTR 6.5 1037 AC M31682 3'UTR 8 1601 AG M31682 3'UTR 6.5 1886 TG M31732 3'UTR 15 1474 C M31899 CDS 5.66 869 GAA M31932 3'UTR 13 1430 T M32315 3'UTR 7.75 1814 TTTG M32315 3'UTR 6.5 3589 TG M32315 3'UTR 12 2368 A M34041 CDS 6.66 903 GAG M34309 5'UTR 6.S 4 CA M34539 3'UTR 12 1120 T M35531 3'UTR 6.25 2068 TTAT M35531 3'UTR 18 1752 T M35663 3'UTR 18 2056 T M36089 UNKNOWN 17 2462 AC M36542 3'UTR 18 1886 A M36711 3'UTR 6.66 1494 GCC M36820 3'UTR 6.25 540 TATT M36860 CDS 3.66 950 CAGCTG M37981 CDS 6.33 113 GCT M54915 5'UTR 3.8 246 CAGCA M54915 5'UTR 9 45 GCA M54915 3'UTR 5.25 2191 TATT M54927 3'UTR 14 2476 A M55047 3'UTR 22.5 2095 GT M55053 3'UTR 12 1915 T M55172 CDS 7.96 3238 CTGCCCCTGGAGTAGAGGACATCAGCGGGCTTCCTTCTG GAGAAGTTCTAGAGACCG (SEQ ID NO:261) M55172 CDS 5.52 2979 GGGCTTCCTTCTGGAGAAGTTCTAGAGACCACTGCCCCT GGAGTAGAGGACATCAGC (SEQ ID NO:262) M55172 CDS 5 3636 GCTGCCCCTGGAGTAGAGGACATCAGCGGGCTTCCTTCT GGAGAAGTTCTAGAGACT (SEQ ID NO:263) M55422 5'UTR 5.66 944 TTG M55542 3'UTR 14 2006 A M55593 5'UTR 7.33 87 GCG M55630 UNKNOWN 22 126 GT M55630 UNKNOWN 12 1538 A M55654 CDS 18.66 466 CAG M55654 CDS 9.66 430 CAG M55654 3'UTR 13 1297 T M55683 3'UTR 12 1203 TG M57627 3'UTR 3.5 1457 AAAAAT M58583 3'UTR 5.66 1354 TTG M59305 5'UTR 4.16 129 CTTTTT M59465 3'UTR 12 3986 A M59499 3'UTR 2.91 2093

TAGCTTCATGAA (SEQ ID NO:264) M59499 3'UTR 15 2248 T M59941 3'UTR 8 2912 AC M60052 CDS 14.33 911 GAT M60052 CDS 8.66 749 GAG M60314 5'UTR 13 637 T M60315 CDS 7 493 AGC M60626 3'UTR 13 1206 A M61108 3'UTR 12 3880 TG M61108 3'UTR 14 4060 T M61877 5'UTR 11.5 123 TC M61877 5'UTR 12 45 T M61877 3'UTR 17.5 7539 GT M62302 UNKNOWN 5.66 1799 GCG M62626 5'UTR 3.6 658 CCCCT M62831 3'UTR 4.75 1112 TTTG M63175 3'UTR 24 1503 T M64347 3'UTR 8 2317 TG M64347 3'UTR 6.5 2831 AT M64716 5'UTR 16 0 T M64930 UNKNOWN 14 3427 A M64936 UNKNOWN 50 3307 A M65131 UNKNOWN 28 2770 A M65290 3'UTR 4.75 2256 TTTA M68520 3'UTR 17 2047 T M69013 3'UTR 12 1386 T M73047 3'UTR 22 4250 T M73531 3'UTR 19 1757 T M73547 3'UTR 26.5 1412 AC M73746 CDS 5.66 73 GCT M74047 3'UTR 19 881 AT M74047 3'UTR 13 1966 T M74491 3'UTR 7 2744 TG M74491 3'UTR 6.5 1124 CT M74525 5'UTR 11.66 296 CGG M74525 5'UTR 12 381 T M74719 5'UTR 7.66 37 GGC M76558 CDS 3.5 2987 GGAAGA M76558 BORDER 7.66 509 GAT M76729 CDS 6.33 294 GCT M77140 3'UTR 12 461 T M77235 3'UTR 7 6773 CA M77498 CDS 3.73 447 GGTGGTTCTGGTGGT (SEQ ID NO:265) M77698 CDS 6 446 CCA M77698 CDS 5.66 366 GAG M77698 3'UTR 13 2018 A M77698 3'UTR 12 1641 A M80482 CDS 3.66 243 GGGCGCGGG M80899 3'UTR 7.5 3857 AT M81601 5'UTR 7.66 0 GCC M83216 CDS 3 1182 GGAGGAAGAGAAAAGGGCAGCAGAGGAGAGGCAGAGGAT AAA (SEQ ID NO:266) M83738 3'UTR 9 2798 TG M83751 CDS 8 256 GGA M84424 3'UTR 8.5 1341 AC M84739 5'UTR 14 25 C M85169 3'UTR 12 1712 T M85590 UNKNOWN 17 0 T M85670 UNKNOWN 13 227 A M86400 3'UTR 18 1632 T M86406 5'UTR 3.57 71 CGCCCGC M86406 3'UTR 6.5 2952 GA M86699 5'UTR 15 8 T M87503 CDS 7 574 AGC M87503 3'UTR 13 1400 T M88108 3'UTR 12 1749 A M88282 3'UTR 7.75 4728 AAAG M88282 3'UTR 16 4715 A M89796 3'UTR 23 2068 A M89796 3'UTR 14 1205 T M90391 CDS 6.66 694 CCT M90656 5'UTR 9.66 55 GGA M91463 3'UTR 23 2202 T

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L30	L29 and l26	3	L30
L29	L28 or l25	78	L29
L28	cek2 or (cek adj 2)	0	L28
L27	(brain or cerebral or (choroid adj plexus) or cerebellum or hypothalmic) same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	4963	L27
L26	glioma$1 or glioblastoma$1 or medulloblastoma$1 or neurocytoma$1 or pinealoma$1 or astrocytoma$1 or ependymona$1 or craniopharyngioma$1	1273	L26
L25	FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor)	78	L25
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L16	L15[ti,ab]	105	L16
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L13	(brain or cerebral or (choroid adj plexus) or cerebellum or hypothalmic) same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	9201	L13
L12	brain same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	8008	L12
L11	L10[ti.ab]	0	L11
L10	cek2 or (cek adj 2) or FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor adj (3 or III))	59	L10
L9	cek2 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	3	L9
L8	L7 and @ad<20010131	3	L8
L7	L6 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	3	L7
L6	cek or (cek adj (2 or II))	62	L6
L5	L4 or l3	16	L5
L4	L2 and @prad<20010131	6	L4
L3	L2 and @ad<20010131	14	L3
L2	L1 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	16	L2
L1	FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor adj (3 or III))	52	L1

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L5: Entry 11 of 16 File: USPT Apr 10, 2001

DOCUMENT-IDENTIFIER: US 6214795 B1
TITLE: Peptide compounds useful for modulating FGF receptor activity

DATE FILED (1):
19961112

Brief Summary Text (4):
The FGFs mediate their effects by binding to high affinity cell surface receptors (reviewed in Johnson and Williams (1992) Adv. Cancer Res. 60:1-41). Four distinct FGF receptors have been identified: FGFR1 (also known was Flg, bFGFR, Cek1 or N-bFGFR) (Lee et al. (1989) Science 245:57-60; Dionne et al. (1990) EMBO J. 9:2685-2692; Johnson et al. (1990) Mol. Cell. Biol. 10:4728-4736; Eisemann et al. (1991) Oncogene 6:1195-1202; Hou et al. (1991) Science 251:665-668), FGFR2 (also known as Bek, Cek3, K-sam, TK14, TK25 or KGFR) (Dionne et al. (1990) EMBO J. 9:2685-2692; Hattori et al. (1990) Proc. Natl. Acad. Sci. USA 87:5983-5987; Miki et al. (1991) Science 251:72-75; Saiki et al. (1988) Science 239:487-491; Pasquale (1990) Proc. Natl. Acad. Sci. USA 87:5812-5816; Houssaint et al. (1990) Proc. Natl. Acad. Sci. USA 87:8180-8184; Champion-Arnaud et al. (1991) Oncogene 6:979-987; Crumley et al. (1991) Oncogene 6:2255-2262; Raz et al. (1991) Oncogene 6:753-760; Sato et al. (1991) Oncogene 6:1279-1283), FGFR3 (also known as Cek2) (Keegan et al. (1991) Proc. Natl. Acad. Sci. USA 88:1095-1099) and FGFR4 (Partanen et al. (1991) EMBO J. 10:1347-1354).

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Proc Natl Acad Sci U S A 1991 Feb 15;88(4):1095-9

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Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3.

Keegan K, Johnson DE, Williams LT, Hayman MJ.

Department of Microbiology, State University of New York, Stony Brook 11794.

The fibroblast growth factors are a family of polypeptide growth factors involved in a variety of activities including mitogenesis, angiogenesis, and wound healing.

Fibroblast growth factor receptors (FGFRs) have previously been identified in chicken, mouse, and human and have been shown to contain an extracellular domain

with either two or three immunoglobulin-like domains, a transmembrane domain, and a cytoplasmic tyrosine kinase domain. We have isolated a human cDNA for

another tyrosine kinase receptor that is highly homologous to the previously described FGFR. Expression of this receptor cDNA in COS cells directs the expression

of a 125-kDa glycoprotein. We demonstrate that this cDNA encodes a biologically active receptor by showing that human acidic and basic fibroblast growth factors

activate this receptor as measured by 45Ca2+ efflux assays. These data establish the existence of an additional member of the FGFR family that we have named

FGFR-3.

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L5: Entry 15 of 16 File: USPT Jul 21, 1998

DOCUMENT-IDENTIFIER: US 5783683 A
TITLE: Antisense oligonucleotides which reduce expression of the FGFRI gene

DATE FILED (1):
19950110

Drawing Description Text (10):
FIG. 9 shows an RT-PCR Southern Blot of FGFR1, FGFR3, and FGFR4 demonstrating the selective reduction of FGFR1 mRNA following treatment of glioblastoma cells with the antisense molecules of the invention.

Detailed Description Text (122):
mRNA was analyzed as described above with the exception that both FGFR1, FGFR3 and FGFR4 mRNA were studied in this particular work. SNB-19 glioblastoma cells were plated at 1.times.10.sup.5 cells per 100 mm dish in serum-supplemented medium. Eighteen hours later the cells were converted to serum-free medium containing FGFR1.alpha. antisense oligonucleotide (R1AS.alpha., 30 .mu.m) or FGFR1.alpha. antisense reverse control oligonucleotide (R1.alpha.RC, 30 .mu.m). Non-treated cells (NT) were run as a control. Cells were treated for three consecutive days with oligonucleotide. Cells were scraped on day 7 and mRNA and cDNA were purified and synthesized respectively. Using cDNA from each of the three different treatments, PCR was used to amplify cDNA for FGFR1, FGFR3, and FGFR4 receptors. SNB-19 cells do not produce FGFR2.

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Brain Tumor Pathol. 2002;19(1):23-9.
PMID: 12455885 [PubMed - indexed for MEDLINE]
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Autocrine signaling through Ras regulates cell survival activity in hu glioma cells: potential cross-talk between Ras and the phosphatidylin 3-kinase-Akt pathway.
Sakata K, Kato S, Fox JC, Shigemori M, Morimatsu M.
J Neuropathol Exp Neurol. 2002 Nov;61(11):975-83.
PMID: 12430714 [PubMed - indexed for MEDLINE]
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Fibroblast growth factor receptor 4 is a target for the zinc-finger transcription factor Ikaros in the pituitary.
Yu S, Asa SL, Ezzat S.
Mol Endocrinol. 2002 May;16(5):1069-78.
PMID: 11981041 [PubMed - indexed for MEDLINE]
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Fibroblast growth factor receptor (FGFR) 4 correlated with the malignancy of human astrocytomas.
Yamada SM, Yamada S, Hayashi Y, Takahashi H, Teramoto A, Matsumc
Neurol Res. 2002 Apr;24(3):244-8.
PMID: 11958417 [PubMed - indexed for MEDLINE]
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Antitumor activity of fibroblast growth factors (FGFs) for medulloblastoma may correlate with FGF receptor expression and tu variant.
Duplan SM, Theoret Y, Kenigsberg RL.
Clin Cancer Res. 2002 Jan;8(1):246-57.

PMID: 11801566 [PubMed - indexed for MEDLINE]
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Targeted expression of a human pituitary tumor-derived isoform of F receptor-4 recapitulates pituitary tumorigenesis.
Ezzat S, Zheng L, Zhu XF, Wu GE, Asa SL.
J Clin Invest. 2002 Jan;109(1):69-78.
PMID: 11781352 [PubMed - indexed for MEDLINE]
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Pituitary adenomas in man and mouse: oncogenic potential of a trun fibroblast growth factor receptor 4.
Low MJ.
J Clin Invest. 2002 Jan;109(1):15-6. No Abstract Available.
PMID: 11781345 [PubMed - indexed for MEDLINE]
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Histological and genetic diagnosis of gliomatosis cerebri: case report.
Yamada SM, Hayashi Y, Takahashi H, Teramoto A, Matsumoto K, Yama
J Neurooncol. 2001 May;52(3):237-40.
PMID: 11519853 [PubMed - indexed for MEDLINE]
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9 ☐ Expand Related Articles
Inhibition of fibroblast growth factor/fibroblast growth factor recept activity in glioma cells impedes tumor growth by both angiogenesis-dependent and -independent mechanisms.
Auguste P, Gursel DB, Lemiere S, Reimers D, Cuevas P, Carceller F, Di S JP, Bikfalvi A.
Cancer Res. 2001 Feb 15;61(4):1717-26.
PMID: 11245488 [PubMed - indexed for MEDLINE]
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Correlation of bFGF, FGFR-1 and VEGF expression with vascularity malignancy of human astrocytomas.
Bian XW, Du LL, Shi JQ, Cheng YS, Liu FX.
Anal Quant Cytol Histol. 2000 Jun;22(3):267-74.
PMID: 10872046 [PubMed - indexed for MEDLINE]
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Suppression of glioblastoma cell growth following antisense oligonucleotide-mediated inhibition of fibroblast growth factor recep expression.
Yamada SM, Yamaguchi F, Brown R, Berger MS, Morrison RS.
Glia. 1999 Oct;28(1):66-76.
PMID: 10498824 [PubMed - indexed for MEDLINE]
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[Inhibition of fibroblast growth factor receptor 1 expression in huma glioblastoma cell contributes to the cell growth suppression]
Yamada SM, Yamaguchi F, Morrison RS, Takahashi H, Teramoto A.
No To Shinkei. 1998 Dec;50(12):1101-5. Japanese.
PMID: 9989355 [PubMed - indexed for MEDLINE]
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Altered expression of fibroblast growth factor receptors in human pituitary adenomas.
Abbass SA, Asa SL, Ezzat S.
J Clin Endocrinol Metab. 1997 Apr;82(4):1160-6.
PMID: 9100589 [PubMed - indexed for MEDLINE]
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[Expression of fibroblast growth factor receptors (FGFRs) mRNA in human astrocytomas]
Yamada SM, Bruner JM, Berger MS, Morrison RS.
No To Shinkei. 1996 Apr;48(4):363-70. Japanese.
PMID: 8679334 [PubMed - indexed for MEDLINE]
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BK1: an FGF-responsive central nervous system-derived cell line.
Benvenisty N, Ornitz DM.
Growth Factors. 1995;12(1):49-55.
PMID: 8527163 [PubMed - indexed for MEDLINE]
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Transfection with bFGF sense and antisense cDNA resulting in modification of malignant glioma growth.
Redekop GJ, Naus CC.
J Neurosurg. 1995 Jan;82(1):83-90.
PMID: 7815139 [PubMed - indexed for MEDLINE]
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Enhanced expression of the tie receptor tyrosine kinase mesenger RN the vascular endothelium of metastatic melanomas.
Kaipainen A, Vlaykova T, Hatva E, Bohling T, Jekunen A, Pyrhonen S, A K.
Cancer Res. 1994 Dec 15;54(24):6571-7.
PMID: 7987857 [PubMed - indexed for MEDLINE]
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Immunohistochemical study for basic fibroblast growth factor and fibroblast growth factor receptor I in pituitary adenomas.
Suzui H, Takahashi JA, Fukumoto M, Hashimoto N, Itoh N, Hatanaka M, Kikuchi H.
Neurosci Lett. 1994 Apr 25;171(1-2):192-6.
PMID: 7916136 [PubMed - indexed for MEDLINE]
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Expression of fibroblast growth factor receptor-1 in human glioma ai meningioma tissues.
Ueba T, Takahashi JA, Fukumoto M, Ohta M, Ito N, Oda Y, Kikuchi H, Hatanaka M.
Neurosurgery. 1994 Feb;34(2):221-5; discussion 225-6.
PMID: 8177381 [PubMed - indexed for MEDLINE]
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Differential expression of two fibroblast growth factor-receptor genes associated with malignant progression in human astrocytomas.
Yamaguchi F, Saya H, Bruner JM, Morrison RS.
Proc Natl Acad Sci U S A. 1994 Jan 18;91(2):484-8.
PMID: 8290551 [PubMed - indexed for MEDLINE]

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Basic fibroblast growth factor and fibroblast growth factor receptor 1 implicated in the growth of human astrocytomas.
Morrison RS, Yamaguchi F, Saya H, Bruner JM, Yahanda AM, Donehow LA, Berger M.
J Neurooncol. 1994;18(3):207-16.
PMID: 7964981 [PubMed - indexed for MEDLINE]
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Identification and characterization of high molecular weight forms of basic fibroblast growth factor in human pituitary adenomas.
Li Y, Koga M, Kasayama S, Matsumoto K, Arita N, Hayakawa T, Sato B
J Clin Endocrinol Metab. 1992 Dec;75(6):1436-41.
PMID: 1464644 [PubMed - indexed for MEDLINE]
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Angiogenic activity of the K-fgf/hst oncogene in neural transplants.
Brustle O, Aguzzi A, Talarico D, Basilico C, Kleihues P, Wiestler OD.
Oncogene. 1992 Jun;7(6):1177-83.
PMID: 1375717 [PubMed - indexed for MEDLINE]
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Phosphorothioate antisense oligonucleotides against basic fibroblast growth factor inhibit anchorage-dependent and anchorage-independ growth of a malignant glioblastoma cell line.
Murphy PR, Sato Y, Knee RS.
Mol Endocrinol. 1992 Jun;6(6):877-84.
PMID: 1323055 [PubMed - indexed for MEDLINE]
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Gene expression of fibroblast growth factor receptors in the tissues of human gliomas and meningiomas.
Takahashi JA, Suzui H, Yasuda Y, Ito N, Ohta M, Jaye M, Fukumoto M, Y, Kikuchi H, Hatanaka M.
Biochem Biophys Res Commun. 1991 May 31;177(1):1-7.
PMID: 1645953 [PubMed - indexed for MEDLINE]
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M64347. Human novel growt...[gi:182564]

Links

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Links

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VERSION NM_000142.2 GI:13112046
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4093)
AUTHORS Partanen,J., Makela,T.P., Alitalo,R., Lehvaslaiho,H. and Alitalo,K.
TITLE Putative tyrosine kinases expressed in K-562 human leukemia cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8913-8917 (1990)
MEDLINE 91062389
PUBMED 2247464
REFERENCE 2 (bases 1 to 4093)
AUTHORS Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
TITLE Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1095-1099 (1991)
MEDLINE 91142118
PUBMED 1847508
REFERENCE 3 (bases 1 to 4093)
AUTHORS Thompson,L.M., Plummer,S., Schalling,M., Altherr,M.R., Gusella,J.F., Housman,D.E. and Wasmuth,J.J.
TITLE A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4
JOURNAL Genomics 11 (4), 1133-1142 (1991)
MEDLINE 92147110
PUBMED 1664411
REFERENCE 4 (bases 1 to 4093)
AUTHORS Velinov,M., Slaugenhaupt,S.A., Stoilov,I., Scott,C.I. Jr., Gusella,J.F. and Tsipouras,P.
TITLE The gene for achondroplasia maps to the telomeric region of chromosome 4p
JOURNAL Nat. Genet. 6 (3), 314-317 (1994)
MEDLINE 94282083
PUBMED 8012397
REFERENCE 5 (bases 1 to 4093)
AUTHORS Le Merrer,M., Rousseau,F., Legeai-Mallet,L., Landais,J.C., Pelet,A., Bonaventure,J., Sanak,M., Weissenbach,J., Stoll,C., Munnich,A. et al.
TITLE A gene for achondroplasia-hypochondroplasia maps to chromosome 4p
JOURNAL Nat. Genet. 6 (3), 318-321 (1994)

MEDLINE 94282084
PUBMED 8012398
REFERENCE 6 (bases 1 to 4093)
AUTHORS Francomano,C.A., Ortiz de Luna,R.I., Hefferon,T.W., Bellus,G.A., Turner,C.E., Taylor,E., Meyers,D.A., Blanton,S.H., Murray,J.C., McIntosh,I. et al.
TITLE Localization of the achondroplasia gene to the distal 2.5 Mb of human chromosome 4p
JOURNAL Hum. Mol. Genet. 3 (5), 787-792 (1994)
MEDLINE 94362678
PUBMED 8081365
REFERENCE 7 (bases 1 to 4093)
AUTHORS Perez-Castro,A.V., Wilson,J. and Altherr,M.R.
TITLE Genomic organization of the human fibroblast growth factor receptor 3 (FGFR3) gene and comparative sequence analysis with the mouse Fgfr3 gene
JOURNAL Genomics 41 (1), 10-16 (1997)
MEDLINE 97271550
PUBMED 9126476
REFERENCE 8 (bases 1 to 4093)
AUTHORS Passos-Bueno,M.R., Wilcox,W.R., Jabs,E.W., Sertie,A.L., Alonso,L.G. and Kitoh,H.
TITLE Clinical spectrum of fibroblast growth factor receptor mutations
JOURNAL Hum. Mutat. 14 (2), 115-125 (1999)
MEDLINE 99355711
PUBMED 10425034
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from M58051.1 and M64347.1.
On Feb 23, 2001 this sequence version replaced gi:4503710.
Summary: The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Alternative splicing occurs and additional variants have been described, including those utilizing alternate exon 8 rather than 9, but their full-length nature has not been determined.
Transcript Variant: This variant (1) is missing alternatively spliced exon 8 but utilizes alternatively spliced exon 9, resulting in isoform (1) with the IIIc-type C-terminal half of the IgIII domain.

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Links

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REFERENCE 1 (bases 1 to 3757)
AUTHORS Partanen,J., Makela,T.P., Alitalo,R., Lehvaslaiho,H. and Alitalo,K.
TITLE Putative tyrosine kinases expressed in K-562 human leukemia cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8913-8917 (1990)
MEDLINE 91062389
PUBMED 2247464
REFERENCE 2 (bases 1 to 3757)
AUTHORS Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
TITLE Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1095-1099 (1991)
MEDLINE 91142118
PUBMED 1847508
REFERENCE 3 (bases 1 to 3757)
AUTHORS Thompson,L.M., Plummer,S., Schalling,M., Altherr,M.R., Gusella,J.F., Housman,D.E. and Wasmuth,J.J.
TITLE A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4
JOURNAL Genomics 11 (4), 1133-1142 (1991)
MEDLINE 92147110
PUBMED 1664411
REFERENCE 4 (bases 1 to 3757)
AUTHORS Velinov,M., Slaugenhaupt,S.A., Stoilov,I., Scott,C.I. Jr., Gusella,J.F. and Tsipouras,P.
TITLE The gene for achondroplasia maps to the telomeric region of chromosome 4p
JOURNAL Nat. Genet. 6 (3), 314-317 (1994)
MEDLINE 94282083
PUBMED 8012397
REFERENCE 5 (bases 1 to 3757)
AUTHORS Le Merrer,M., Rousseau,F., Legeai-Mallet,L., Landais,J.C., Pelet,A., Bonaventure,J., Sanak,M., Weissenbach,J., Stoll,C., Munnich,A. et al.
TITLE A gene for achondroplasia-hypochondroplasia maps to chromosome 4p
JOURNAL Nat. Genet. 6 (3), 318-321 (1994)

MEDLINE 94282084
PUBMED 8012398
REFERENCE 6 (bases 1 to 3757)
AUTHORS Francomano,C.A., Ortiz de Luna,R.I., Hefferon,T.W., Bellus,G.A., Turner,C.E., Taylor,E., Meyers,D.A., Blanton,S.H., Murray,J.C., McIntosh,I. et al.
TITLE Localization of the achondroplasia gene to the distal 2.5 Mb of human chromosome 4p
JOURNAL Hum. Mol. Genet. 3 (5), 787-792 (1994)
MEDLINE 94362678
PUBMED 8081365
REFERENCE 7 (bases 1 to 3757)
AUTHORS Perez-Castro,A.V., Wilson,J. and Altherr,M.R.
TITLE Genomic organization of the human fibroblast growth factor receptor 3 (FGFR3) gene and comparative sequence analysis with the mouse Fgfr3 gene
JOURNAL Genomics 41 (1), 10-16 (1997)
MEDLINE 97271550
PUBMED 9126476
REFERENCE 8 (bases 1 to 3757)
AUTHORS Passos-Bueno,M.R., Wilcox,W.R., Jabs,E.W., Sertie,A.L., Alonso,L.G. and Kitoh,H.
TITLE Clinical spectrum of fibroblast growth factor receptor mutations
JOURNAL Hum. Mutat. 14 (2), 115-125 (1999)
MEDLINE 99355711
PUBMED 10425034
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF245114.1 and M64347.1.
Summary: The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Alternative splicing occurs and additional variants have been described, including those utilizing alternate exon 8 rather than 9, but their full-length nature has not been determined.
Transcript Variant: This variant (2) does not contain alternatively spliced exons 8 or 9, resulting in a loss of the C-terminal half of the IgIII domain. In addition, this variant is missing alternatively spliced exon 10 which encodes the transmembrane region, suggesting a soluble receptor.

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  AUTHORS   Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
  TITLE     Isolation of an additional member of the fibroblast growth factor
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  TITLE     Fibroblast growth factor receptor 3 (FGFR3) genomic sequence
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  TITLE     Fibroblast growth factor receptor 3 lacking the Ig IIIb and
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  AUTHORS   Terada,M., Shimizu,A. and Seo,M.
  TITLE     Secretion and dimerization of the FGFR3 isoform, resulting from
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>gi|7533124|gb|AF245114.1| Homo sapiens fibroblast growth factor receptor 3 (FGFR3) mRNA,
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Length = 2184

Score = 2397 bits (1209), Expect = 0.0
Identities = 1215/1217 (99%)
Strand = Plus / Plus

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>gi|20452379|gb|AF487554.1| Homo sapiens fibroblast growth factor receptor 3 (FGFR3) gene, partial
cds, alternatively spliced
Length = 16976

Score = 1146 bits (578), Expect = 0.0
Identities = 602/611 (98%), Gaps = 1/611 (0%)
Strand = Plus / Plus

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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 20:01:05 ON 18 JAN 2003

L1 8 S M64347###
L2 7 DUP REM L1 (1 DUPLICATE REMOVED)
L3 7949 S (FGF(W)R) OR (FGF(W)R3) OR (FIBROBLAST(W)GROWTH(W)FACTOR(W)(R
L4 115579 S NEUROCYTOMA# OR PINEALOMA# OR GLIOMA# OR MEDULLOBLASTOMA# OR
L5 132127 S (CEREBRAL OR (CHOROID(W)PLEXUS) OR CEREBELLUM OR HYPOTHALAMIC
L6 10081 S (CEREBRAL OR (CHOROID(W)PLEXUS) OR CEREBELLUM OR HYPOTHALAMIC
L7 204265 S L4 OR L5 OR L6
L8 151 S L3 AND L7
L9 115 S L8 AND PY<2001
L10 136 S L8 AND PY<2002
L11 67 DUP REM L10 (69 DUPLICATES REMOVED)
L12 1822 S (FGFR3 OR (FGF(W)R3) OR (FGF(W)RECEPTOR(W)3) OR (FIBROBLAST(W
L13 15 S L12 AND L7
L14 6 DUP REM L13 (9 DUPLICATES REMOVED)
L15 31656 S GOLUB?/AU OR LANDER?/AU OR POMEROY?/AU OR TAMAYO?/AU
L16 0 S L15 AND L8
L17 1 S L15 AND L12
L18 10 S L15 AND L3
L19 10 S L17 OR L18
L20 4 DUP REM L19 (6 DUPLICATES REMOVED)

10/ 066,305

L2 ANSWER 5 OF 7 MEDLINE
ACCESSION NUMBER: 2000408205 MEDLINE
DOCUMENT NUMBER: 20349276 PubMed ID: 10889045
TITLE: Repeat polymorphisms within gene regions: phenotypic and evolutionary implications.
AUTHOR: Wren J D; Forgacs E; Fondon J W 3rd; Pertsemlidis A; Cheng S Y; Gallardo T; Williams R S; Shohet R V; Minna J D; Garner H R
CORPORATE SOURCE: Program in Genetics, Southwestern Graduate School of Biomedical Sciences, Dallas, TX, USA.
CONTRACT NUMBER: P50CA70907 (NCI)
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (2000 Aug) 67 (2) 345-56.
Journal code: 0370475. ISSN: 0002-9297.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF013956; GENBANK-AF017789; GENBANK-AF032886; GENBANK-AF042838; GENBANK-AF047437; GENBANK-AF060231; GENBANK-D14838; GENBANK-D83492; GENBANK-D86407; GENBANK-D86550; GENBANK-L08835; GENBANK-M55047; GENBANK-M60052; GENBANK-M60315; GENBANK-**M64347**; GENBANK-R12160; GENBANK-R42196; GENBANK-T47177; GENBANK-T62484; GENBANK-T63962; GENBANK-T70173; GENBANK-U49020; GENBANK-U60325; GENBANK-X55313; GENBANK-X70811; GENBANK-X78261; GENBANK-X82209; GENBANK-Y00285; GENBANK-Y11525; +
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000901
Last Updated on STN: 20030105
Entered Medline: 20000821

AB We have developed an algorithm that predicted 11,265 potentially polymorphic tandem repeats within transcribed sequences. We estimate that 22% (2,207/9,717) of the annotated clusters within UniGene contain at least one potentially polymorphic locus. Our predictions were tested by allelotyping a panel of approximately 30 individuals for 5% of these regions, confirming polymorphism for more than half the loci tested. Our study indicates that tandem-repeat polymorphisms in genes are more common than is generally believed. Approximately 8% of these loci are within coding sequences and, if polymorphic, would result in frameshifts. Our catalogue of putative polymorphic repeats within transcribed sequences comprises a large set of potentially phenotypic or disease-causing loci. In addition, from the anomalous character of the repetitive sequences within unannotated clusters, we also conclude that the UniGene cluster count substantially overestimates the number of genes in the human genome.

We hypothesize that polymorphisms in repeated sequences occur with some baseline distribution, on the basis of repeat homogeneity, size, and sequence composition, and that deviations from that distribution are indicative of the nature of selection pressure at that locus. We find evidence of selective maintenance of the ability of some genes to respond very rapidly, perhaps even on intragenerational timescales, to fluctuating selective pressures.

L2 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:758742 CAPLUS
DOCUMENT NUMBER: 135:314390
TITLE: Large-scale monitoring of expression patterns of p53-regulated gene and analysis of p53 gene function
INVENTOR(S): Mack, David H.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 46 pp., Cont.-in-part of Appl. No. PCT/US98/01206.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6303301	B1	20011016	US 1998-86285	19980529
WO 9830722	A1	19980716	WO 1998-US1206	19980112

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

US 2002028454	A1	20020307	US 2001-836278	20010418

PRIORITY APPLN. INFO.:

US 1997-35327P	P	19970113
WO 1998-US1206	A2	19980112
US 1997-49627P	P	19970613
US 1998-86285	A3	19980529

AB This invention provides methods, compns. and app. for mapping the regulatory relationships of genes by massive parallel monitoring of gene expression. The information obtained can be of use in drug discovery (no data). The method uses high d. oligonucleotide arrays to monitor changes in expression in response to events and stimuli. Very large nos. of gene (>6,500) may be monitored in this method using samples from many tissues and developmental or disease stages. Changes are quantified and a relationship model constructed using LISREL (Linear Structure Relationship) methods. Mutations in up-stream regulatory genes can be detected by monitoring the change in down-stream gene expression. Similarly, the effect of a specific mutation in an up-stream gene is detd. by monitoring the down-stream gene expression. In addn., regulatory function of a target gene can be detd. by monitoring the expression of a large no. of down-stream genes. The invention also provides specific embodiments for detecting p53 functional homozygous and heterozygous mutations and for detg. the function of p53 mutations.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:241013 CAPLUS
DOCUMENT NUMBER: 136:277466
TITLE: Expressed gene sets as markers for specific tumors
INVENTOR(S): Ramaswamy, Sridhar; Golub, Todd B.; Tamayo, Pablo; Angelo, Michael
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Dana-Farber Cancer Institute, Inc.
SOURCE: PCT Int. Appl., 715 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002024956	A2	20020328	WO 2001-US29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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WO 2002024956	A2	20020328	WO 2001-XB29287	20010919
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WO 2002024956	A2	20020328	WO 2001-XC29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

AU 2001092802	A5	20020402	AU 2001-92802		20010919
US 2002110820	A1	20020815	US 2001-955920		20010919
PRIORITY APPLN. INFO.:			US 2000-233534P	P	20000919
			US 2001-278749P	P	20010326
			WO 2001-US29287	W	20010919

AB Sets of genetic markers for specific tumor classes are described, as well as methods of identifying a biol. sample based on these markers. Total RNA was isolated from .apprx.300 human tumor and normal tissue specimens representing 30 individual classes of tumor or normal tissue, and cDNA produced using established mol. biol. protocols was hybridized to two high d. Affymetrix oligonucleotide microarrays (Hu6800FL and Hu35KsubA0). Raw expression data was combined into a master data set contg. the expression values for between 6800 and 16,000 genes expressed by each individual sample. A filter was applied to this data set which only allows those genes expressed at 3-fold above baseline and with an abs. difference in expression value of 100 to pass. By comparing the sets of genes which are expressed specifically in one class of tumor (e.g., pancreatic adenocarcinoma) vs. its accompanying normal tissue (e.g., normal pancreas), sets of genes were detd. which are specific to various tumors and their normal tissue counterparts. Also described are diagnostic, prognostic, and therapeutic screening uses for these markers, as well as oligonucleotide arrays comprising these markers. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L2 ANSWER 2 OF 7 CAPLUS

L2 ANSWER 7 OF 7 MEDLINE DUPLICATE 1

ACCESSION NUMBER: 92147110 MEDLINE
DOCUMENT NUMBER: 92147110 PubMed ID: 1664411
TITLE: A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4.
AUTHOR: Thompson L M; Plummer S; Schalling M; Altherr M R; Gusella J F; Housman D E; Wasmuth J J
CORPORATE SOURCE: Department of Biological Chemistry, College of Medicine, University of California, Irvine 92717.
CONTRACT NUMBER: NS25631-04 (NINDS)
SOURCE: GENOMICS, (1991 Dec) 11 (4) 1133-42.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-**M64347**
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920405
Last Updated on STN: 20000303
Entered Medline: 19920313

AB The gene responsible for Huntington disease (HD), an autosomal dominant neurodegenerative disorder, is located near the terminus of the short arm of chromosome 4. Detailed genetic linkage and physical mapping studies have defined a region of approximately 2.5 million basepairs where the disease gene is likely to be located. Efforts to identify the disease gene are now focused on the identification and characterization of expressed genes in this region. Nucleotide sequence analysis of a cDNA clone derived from the HD gene region has revealed that it encodes a member of the fibroblast growth factor subfamily of tyrosine kinase receptors, some members of which are known to be involved in the differentiation and survival of certain cell types within the central nervous system. Histochemical analysis using in situ hybridization revealed its expression in many areas of the brain, among them being the caudate and putamen. The nature of this gene, FGFR3, and its map location make it a possible candidate for the HD gene.

L2 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:641026 CAPLUS
DOCUMENT NUMBER: 131:267987
TITLE: Cancer diagnosis and therapy based on expression levels of p53-regulated genes
INVENTOR(S): Levine, Arnold J.; Murphy, Maureen E.; Mack, David H.; Gish, Kurt C.; Tom, Edward Yat Wah
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Princeton University
SOURCE: PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9950456	A1	19991007	WO 1999-US6656	19990326
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6020135	A	20000201	US 1998-49025	19980327
CA 2324444	AA	19991007	CA 1999-2324444	19990326
AU 9932085	A1	19991018	AU 1999-32085	19990326
EP 1064404	A1	20010103	EP 1999-914184	19990326
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6171798	B1	20010109	US 1999-442039	19991117
US 2001039013	A1	20011108	US 2001-755028	20010108

PRIORITY APPLN. INFO.:
US 1998-49025 A1 19980327
WO 1999-US6656 W 19990326
US 1999-442039 A3 19991117

AB Many genes are identified as being p53-regulated which were not heretofore known to be p53-regulated. This includes both genes whose expression is induced and genes whose expression is repressed by the expression of wild-type p53. The effects of p53 expression on gene expression in Eb-1 cells was tested by hybridizing to a chip that contains deoxyoligonucleotide sequences (25-mers) that derived from a database of 6800 known genes or EST sequences. Seventy genes were induced by p53 and 77 were repressed by p53. Monitoring expression of these genes is used to provide indications of p53 status in a cell. Such monitoring can also be used to screen for useful anticancer therapeutics, as well as for substances which are carcinogenic. Defects in p53 can be bypassed by supplying p53 induced genes to cells. Defects in p53 can also be bypassed by supplying antisense constructs to p53-repressed genes.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 66 OF 67 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:79455 CAPLUS
DOCUMENT NUMBER: 114:79455
TITLE: Suppression of basic fibroblast growth factor expression by antisense oligodeoxynucleotides inhibits the growth of transformed human astrocytes
AUTHOR(S): Morrison, Richard S.
CORPORATE SOURCE: Robert S. Dow Neurol. Sci. Inst., Good Samaritan Hosp., Portland, OR, 97209, USA
SOURCE: Journal of Biological Chemistry (**1991**), 266(2), 728-34
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Basic fibroblast growth factor (bFGF) is a heparin-binding protein expressing potent mitogenic and angiogenic properties. Elevated levels of bFGF have recently been described in human **glioma** cell lines. The high degree of vascularity and invasiveness which characterize human **gliomas** suggest that activated expression of bFGF or similar proteins may be related to the aberrant growth patterns of these tumors. The influence of endogenous bFGF on **glioma** cell growth in vitro was evaluated in the present study by downregulating bFGF expression using antisense oligonucleotide primers. The addn. of 50 .mu.M bFGF-specific antisense primer to the human **glioma** cell line SNB-19 resulted in an 80% inhibition in **glioma** growth. This effect was saturable and specific. Antisense primers directed to 2 different sites of bFGF mRNA were effective in suppressing SNB-19 growth, whereas sense strand primer was ineffective. Furthermore, only the antisense primer significantly reduced the specific activity of bFGF protein in SNB-19 cell exts. Neither antisense or sense primers inhibited the growth of non-transformed human glia. BFGF mRNA was detected in both transformed and nontransformed human glia by polymerase chain reaction anal. suggesting that alterations in bFGF isoform content or activity may be specifically related to abnormal growth control in human **gliomas**.

L11 ANSWER 65 OF 67 MEDLINE DUPLICATE 26

ACCESSION NUMBER: 91342665 MEDLINE
DOCUMENT NUMBER: 91342665 PubMed ID: 1652059
TITLE: The human **fibroblast growth factor receptor** genes: a common structural arrangement underlies the mechanisms for generating receptor forms that differ in their third immunoglobulin domain.
AUTHOR: Johnson D E; Lu J; Chen H; Werner S; Williams L T
CORPORATE SOURCE: Howard Hughes Medical Institute, Program of Excellence in Molecular Biology, University of California, San Francisco 94143-0724.
CONTRACT NUMBER: HL-43821 (NHLBI)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, **(1991 Sep)** 11 (9) 4627-34.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199109
ENTRY DATE: Entered STN: 19911013
Last Updated on STN: 19970203
Entered Medline: 19910920

AB To determine the mechanisms by which multiple forms of fibroblast growth factor (FGF) receptors are generated, we have mapped the arrangement of exons and introns in the human FGF receptor 1 (FGFR 1) gene (flg). We found three alternative exons encoding a portion of the third immunoglobulin (Ig)-like domain of the receptor. One of these alternatives encodes a sequence that is part of a secreted form of FGFR 1. The other two encode sequences that are likely part of transmembrane forms of FGFR 1. One of these forms has not been previously reported in published cDNAs.

Also, we have determined the structural organization of a portion of the human FGFR 2 gene (bek) and found a similar arrangement of alternative exons for the third Ig-like domain. The arrangement of these genes suggests that there are conserved mechanisms governing the expression of secreted FGF receptors as well as the expression of at least two distinct membrane-spanning forms of the FGF receptors. The diverse forms appear to be generated by alternative splicing of mRNA and selective use of polyadenylation signals.

L14 ANSWER 6 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 97229252 MEDLINE
DOCUMENT NUMBER: 97229252 PubMed ID: 9075249
TITLE: Pediatric **brain tumors** express multiple receptor tyrosine kinases including novel cell adhesion kinases.
AUTHOR: Weiner H L; Rothman M; Miller D C; Ziff E B
CORPORATE SOURCE: Department of Neurosurgery (Pediatric Neurosurgery), New York University Medical Center, NY 10016, USA.
CONTRACT NUMBER: P20 NS31088 (NINDS)
SOURCE: PEDIATRIC NEUROSURGERY, (1996 Aug) 25 (2) 64-71; discussion 71-2.
Journal code: 9114967. ISSN: 1016-2291.
PUB. COUNTRY: Switzerland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970612
Last Updated on STN: 20000303
Entered Medline: 19970603

AB We have used the polymerase chain reaction to clone and characterize growth factor receptor tyrosine kinases (RTKs) expressed in 3 pathologically distinct pediatric **brain tumors**, an anaplastic **ependymoma**, a glioblastoma multiforme and a primitive neuroectodermal tumor (PNET). These neoplasms are presumed to be derived from embryonic neuroepithelial precursor cells of the central nervous system. This cloning demonstrated expression of 24 distinct kinase genes: 16 receptor type kinases and 8 nonreceptor type kinases. The expression of 6 receptors, including Hek2, IRR, Ryk, **FGFR3**, and 2 members of the newly identified cell adhesion kinase receptor family, DDR and TKT, in such tumors has not been reported previously. Northern analysis of mRNA levels revealed DDR expression in 6 of 7 pediatric **brain tumors** including an **ependymoma**, PNET, glioblastoma and **astrocytoma**, and also in an adult pheochromocytoma. Thus, the DDR cell adhesion kinase may be widely expressed in pediatric **brain tumors**. Also, PCR cloning may be an effective procedure for characterizing RTKs in clinical tissue samples and revealing the expression of novel RTK species.

WER 5 OF 6 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 1999085118 MEDLINE
DOCUMENT NUMBER: 99085118 PubMed ID: 9864407
TITLE: Fibroblast growth factor-9 (glia-activating factor) stimulates proliferation and production of glial fibrillary acidic protein in human **gliomas** either in the presence or in the absence of the endogenous growth factor expression.
AUTHOR: Miyagi N; Kato S; Terasaki M; Aoki T; Sugita Y; Yamaguchi M; Shigemori M; Morimatsu M
CORPORATE SOURCE: Department of Pathology, Kurume University, School of Medicine, Kurume, Japan.
SOURCE: ONCOLOGY REPORTS, (1999 Jan-Feb) 6 (1) 87-92. Journal code: 9422756. ISSN: 1021-335X.
PUB. COUNTRY: Greece
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 19990402
Entered Medline: 19990322

AB We tested fibroblast growth factor-9 (FGF-9) expression in human **glioma** cells (U251MG, T98G, U87MG, KALS-1, NMC-G1) and only NMC-G1 expressed endogenous FGF-9. All cells expressed bFGF and high affinity receptors for FGFs (FGFR1 and **FGFR3**). Exogenously supplied bFGF and FGF-9 both showed mitogenic activities in all cells. Neutralizing antibody against bFGF inhibited the proliferation in U251MG and NMC-G1, however that against FGF-9 inhibited the proliferation only in NMC-G1. GFAP expression was stimulated by both FGFs in these cells. FGF-9 potentially regulates proliferation and GFAP expression in human **gliomas** either in the presence or in the absence of the endogenous growth factor expression.

L14 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:756373 CAPLUS
DOCUMENT NUMBER: 136:51990
TITLE: Expression profiling of **medulloblastoma**: PDGFRA and the RAS/MAPK pathway as therapeutic targets for metastatic disease
AUTHOR(S): MacDonald, Tobey J.; Brown, Kevin M.; LaFleur, Bonnie; Peterson, Katia; Lawlor, Christopher; Chen, Yidong; Packer, Roger J.; Cogen, Philip; Stephan, Dietrich A.
CORPORATE SOURCE: Center for Cancer and Transplantation Biology, Children's National Medical Center, Washington, DC, USA
SOURCE: Nature Genetics (2001), 29(2), 143-152
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature America Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Little is known about the genetic regulation of **medulloblastoma** dissemination, but metastatic **medulloblastoma** is highly assocd. with poor outcome. We obtained expression profiles of 23 primary **medulloblastomas** clin. designated as either metastatic (M+) or non-metastatic (M0) and identified 85 genes whose expression differed significantly between classes. Using a class prediction algorithm based on these genes and a leave-one-out approach, we assigned sample class to these tumors (M+ or M0) with 72% accuracy and to four addnl. independent tumors with 100% accuracy. We also assigned the metastatic **medulloblastoma** cell line Daoy to the metastatic class. Notably, platelet-derived growth factor receptor .alpha. (PDGFRA) and members of the downstream RAS/mitogen-activated protein kinase (MAPK) signal transduction pathway are upregulated in M+ tumors. Immunohistochem. validation on an independent set of tumors shows significant overexpression of PDGFRA in M+ tumors compared to M0 tumors. Using in vitro assays, we show that platelet-derived growth factor .alpha. (PDGFA) enhances **medulloblastoma** migration and increases downstream MAP2K1 (MEK1), MAP2K2 (MEK2), MAPK1 (p42 MAPK) and MAPK3 (p44 MAPK) phosphorylation in a dose-dependent manner. Neutralizing antibodies to PDGFRA blocks MAP2K1, MAP2K2 and MAPK1/3 phosphorylation, whereas U0126, a highly specific inhibitor of MAP2K1 and MAP2K2, also blocks MAPK1/3. Both inhibit migration and prevent PDGFA-stimulated migration. These results provide the first insight into the genetic regulation of **medulloblastoma** metastasis and are the first to suggest a role for PDGFRA and the RAS/MAPK signaling pathway in **medulloblastoma** metastasis. Inhibitors of PDGFRA and RAS proteins should therefore be considered for investigation as possible novel therapeutic strategies against **medulloblastoma**.

REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:265659 BIOSIS
DOCUMENT NUMBER: PREV200100265659
TITLE: Crystal structure of fibroblast growth factor 9 reveals regions implicated in dimerization and autoinhibition.
AUTHOR(S): Plotnikov, Alexander N.; Eliseenkova, Anna V.; Ibrahimi, Omar A.; Shriver, Zachary; Sasisekharan, Ram; Lemmon, Mark A.; Mohammadi, Moosa (1)
CORPORATE SOURCE: (1) Department of Pharmacology, New York University School of Medicine, New York, NY, 10016 USA
SOURCE: Journal of Biological Chemistry, (February 9, 2001) Vol. 276, No. 6, pp. 4322-4329. print.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Fibroblast growth factors (FGFs) constitute a large family of heparin-binding growth factors with diverse biological activities. FGF9 was originally described as glia-activating factor and is expressed in the nervous system as a potent mitogen for glia cells. Unlike most FGFs, FGF9 forms dimers in solution with a Kd of 680 nM. To elucidate the molecular mechanism of FGF9 dimerization, the crystal structure of FGF9 was determined at 2.2 ANG resolution. FGF9 adopts a beta-trefoil fold similar to other FGFs. However, unlike other FGFs, the N- and C-terminal regions outside the beta-trefoil core in FGF9 are ordered and involved in the formation of a 2-fold crystallographic dimer. A significant surface area (>2000 ANG2) is buried in the dimer interface that occludes a major receptor binding site of FGF9. Thus, we propose an autoinhibitory mechanism for FGF9 that is dependent on sequences outside of the beta-trefoil core. Moreover, a model is presented providing a molecular basis for the preferential affinity of FGF9 toward **FGFR3**.

L14 ANSWER 2 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001416780 MEDLINE
DOCUMENT NUMBER: 21359863 PubMed ID: 11466624
TITLE: Frequency of **fibroblast growth factor receptor 3** mutations in sporadic tumours.
AUTHOR: Sibley K; Stern P; Knowles M A
CORPORATE SOURCE: ICRF Clinical Centre, St. James's University Hospital, Leeds, LS9 7TF, UK.
SOURCE: ONCOGENE, (2001 Jul 19) 20 (32) 4416-8. Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20010813
Entered Medline: 20010809

AB Mutations in **FGFR3** have been identified in several tumour types including bladder carcinoma, cervical carcinoma, and multiple myeloma. In bladder carcinoma, we recently identified **FGFR3** mutations in 41% of tumours, making this the most frequently mutated putative oncogene identified in bladder cancer to date. We have now investigated the frequency of **FGFR3** mutation in a panel of 125 tumours and 13 cell lines from various other organs. We analysed the mutation hotspots in exons 7, 10 and 15 by direct DNA sequencing, and found one mutation in exon 7 (S249C) in 1/28 (3.5%) cervical tumours. Mutations were not detected in stomach, rectum, colon, prostate, ovarian, breast, **brain**, or renal **tumours**, nor were they found in any of the cell lines included in this study. We conclude that **FGFR3** is commonly mutated in bladder carcinoma and only rarely in cervical carcinoma. Several tumour types appear not to possess any mutations in **FGFR3**, suggesting that these mutations are important only in the development of certain types of tumour.

L20 ANSWER 3 OF 4 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1999308632 MEDLINE
DOCUMENT NUMBER: 99308632 PubMed ID: 10380925
TITLE: Diverse signaling pathways activated by growth factor receptors induce broadly overlapping, rather than independent, sets of genes.
COMMENT: Comment in: Cell. 1999 Jun 11;97(6):675-8
AUTHOR: Fambrough D; McClure K; Kazlauskas A; **Lander E S**
CORPORATE SOURCE: Whitehead Institute for Biomedical Research, Cambridge, Massachusetts 02142, USA.
SOURCE: CELL, (1999 Jun 11) 97 (6) 727-41.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990730
Last Updated on STN: 20000303
Entered Medline: 19990722

AB We sought to explore the relationship between receptor tyrosine kinase (RTK) activated signaling pathways and the transcriptional induction of immediate early genes (IEGs). Using global expression monitoring, we identified 66 fibroblast IEGs induced by platelet-derived growth factor beta receptor (PDGFRbeta) signaling. Mutant receptors lacking binding sites for activation of the PLCgamma, PI3K, SHP2, and RasGAP pathways still retain partial ability to induce 64 of these IEGs. Removal of the Grb2-binding site further broadly reduces induction. These results suggest that the diverse pathways exert broadly overlapping effects on IEG induction. Interestingly, a mutant receptor that restores the RasGAP-binding site promotes induction of an independent group of genes, normally induced by interferons. Finally, we compare the PDGFRbeta and **fibroblast growth factor receptor** 1; each induces essentially identical IEGs in fibroblasts.

L14 ANSWER 32 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2001064882 PCTFULL ED 20020822
TITLE (ENGLISH): 1983, 52881, 2398, 45449, 50289, AND 52872, G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
TITLE (FRENCH): RECEPTEURS COUPLES A UNE PROTEINE G, NUMEROTEES 1983, 52881, 2398, 45449, 50289, ET 52872, ET UTILISATIONS CORRESPONDANTES
INVENTOR(S): GLUCKSMANN, Maria, Alexandra; GALVIN, Katherine, M.; SILOS-SANTIAGO, Inmaculada
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC.; GLUCKSMANN, Maria, Alexandra; GALVIN, Katherine, M.; SILOS-SANTIAGO, Inmaculada
DOCUMENT TYPE: Patent
PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2001064882	A2	20010907

DESIGNATED STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG

APPLICATION INFO.:	WO 2001-US6543	A	20010228
PRIORITY INFO.:	US 2000-60/186,059		20000229

DETD The subject can be a cancer patient e.g., a patient with **brain cancer**, bone **cancer**, or prostate cancer. In other embodiments, the subject is a non-human anirrial, elg., an experimental animal, e.g., an aithritic rat niodel of. . . . . is a method of evaluating a sample. The method includes providing a sample, e.g., from the subject, and determining a gene **expression profile** of the sample, wherein the profile includes a value representing the level of 1983, 52881, 2398, 45449, 50289and52872expression. ThemethodcanfLirtherincludecoiilparingthevalueo rtf-le profile (i.e., multiple values) to a reference value or reference profile. The gene **expression profile** of the sample can be obtained by any of the methods described herein 1 5 (e.g., by providing a nucleic acid. . . an indication that the subject has or is disposed to having a disorders as described herein. The method can be used to **monitor** a **treatment** for such disorders in a subject. For example, the gene **expression profile** can be determined for a sample from a subject undergoing **treatment**.

L14 ANSWER 22 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2001083781 PCTFULL ED 20020826
TITLE (ENGLISH): 14094, A NOVEL HUMAN TRYPSIN FAMILY MEMBER AND USES THEREOF
TITLE (FRENCH): 14094, UN NOUVEAU MEMBRE DANS LA FAMILLE DE LA TRYPSINE
HUMAINE ET SON UTILISATION
INVENTOR(S): MEYERS, Rachel; MACBETH, Kyle, J.
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC.; MEYERS, Rachel; MACBETH, Kyle, J.
DOCUMENT TYPE: Patent
PATENT INFORMATION:

	NUMBER	KIND	DATE
	WO 2001083781	A2	20011108
DESIGNATED STATES	AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG		
APPLICATION INFO.:	WO 2001-US13903	A	20010430
PRIORITY INFO.:	US 2000-60/200,621		20000428
	US 2000-09/633,300		20000808

DETD . . . cancerous or pre-cancerous tissue where a 14094 polypeptide or nucleic acid is expressed, e.g., breast, ovanian, colon, liver, lung, kldney, or **brain cancer**.

. . .
found in a tissue 1,vhere a 14094 polypeptide or nucieic acid is expressed, e.g., breast, ovarian, colon, liver, lung, kjdney, or **brain cancer**.

. . .
cancer is a sarcoma, a carcinoma, or an adenocarcm'oma. Preferably, the cancer is a breast, ovarian, colon, lung, liver, kidney, or **brain cancer**.

. . .
gastric cancer, esophageal cancer, rectal
5 cancer, pancreatic cancer, ovarian cancer, prostate cancer, utenne cancer, cancer of the head
and neck, skin **cancer, brain cancer,**
squamous cell carcinoma, sebaceous gland carcinoma.

. . .
can further inciude compar-ing the value or the profile (1.e., multiple values) to a
reference value or reference profile. The gene **expression profile** of the sample can be
obtained by any of the methods described herein (e.g., by providing a nuclele acid from the
sample. . . is an
indication that the subject has or is disposed to having a cell proliferative disorder. The
method can be used to **monitor** a **treatment** for a cell
protiferative disorder in a subject. For
example, the gene **expression profile** can be

determined for a sample from a subject
75 -
undergoing **treatment**. The profile can be compared to a
reference profile or to a profile
obtained from the subject prior to **treatment** or prior to onset
of the disorder (see, e.g., Golub
et al. (I 999) Science 286:53 I).

. . .

context,
thc off@LjL of one cell type on another cell type in response to a
biological stimulus can be
determined, e,g., to **monitor** the effect of cell-cell
interaction at the level of gene expression,
In another embodiment, cells are contacted With a **therapeutic**
agent. The
expression profile of the celis is determined using
the array, and the **expression profile** is
compared to the profile of llke celis not contacted ivith the agent.
For
example, the assay
can be used to determine or analyze the molecular basis of an
undesirable effect of the
therapeutic agent. lf an agent is administered
therapeutically to treat one cell type but has an
undesirable effect on another cell type, the invention provides an
assay
to determine. . .

L8 ANSWER 12 OF 20 MEDLINE
ACCESSION NUMBER: 2001393249 MEDLINE
DOCUMENT NUMBER: 21064203 PubMed ID: 11122874
TITLE: Application of advances in molecular biology to the **treatment** of brain tumors.
AUTHOR: Takeshima H; Sawamura Y; Gilbert M R; Van Meir E G
CORPORATE SOURCE: Department of Neurosurgery, Faculty of Medicine, Kagoshima University, 8-35-1 Sakuraga-oka, Kagoshima 890-8520, Japan.. m2040k@khosp2.kufm.kagoshima-u.ac.jp
SOURCE: Curr Oncol Rep, (2000 Sep) 2 (5) 425-33. Ref: 56
Journal code: 100888967. ISSN: 1523-3790.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010716
Last Updated on STN: 20010716
Entered Medline: 20010712

AB Recent advances in molecular biology have substantially improved our understanding of the molecular genetics of primary brain neoplasms. Soon each histopathologic category of glioma will be further divided into subgroups according to similar genetic background, gene **expression profile**, and similarity of biologic responses to radiotherapy or chemotherapy. Identification of key molecules that are specifically altered in neoplastic cells will provide candidate molecular targets for tumor **treatment**. Novel **therapeutic** tools for targeting tumor cells, such as viral vectors for gene **therapy**, have been created. In the near future, the accumulation of new knowledge in brain tumor biology and genetics, combined with rational drug design, will revolutionize the **treatment** of malignant gliomas, which are among the most lethal human cancers.

L14 ANSWER 3 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2002059610 PCTFULL ED 20020809 EW 200231
TITLE (ENGLISH): USING OVEREXPRESSION OF LAMININ ALPHA 4 SUBUNIT AS A DIAGNOSTIC AND PROGNOSTIC INDICATOR OF MALIGNANT TUMORS
TITLE (FRENCH): UTILISATION DE LA SUREXPRESSION DE LA SOUS-UNITE DE LAMININE ALPHA 4 EN TANT QU'INDICATEUR DIAGNOSTIQUE ET PRONOSTIQUE DE TUMEURS MALIGNES
INVENTOR(S): LJUBIMOVA, Julia, Y.; LJUBIMOV, Alexander, V.; BLACK, Keith, L.
PATENT ASSIGNEE(S): CEDARS-SINAI MEDICAL CENTER
AGENT: STEINBERG, Nisan, A., Ph.D.
LANGUAGE OF FILING: English
LANGUAGE OF PUBL.: English
DOCUMENT TYPE: Patent
PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2002059610	A2	20020801

DESIGNATED STATES AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
APPLICATION INFO.: WO 2001-US50292 A 20011219
PRIORITY INFO.: US 2000-09/741,550 20001219
ABEN Disclosed is a method of diagnosing the presence of a malignant tumor, including a glioma, in a human subject, which involves detecting overexpression of laminin *4 subunit protein or laminin *4-specific mRNA, compared to the expression level in a normal tissue control. Also disclosed are a method of predicting the recurrence of a malignant tumor in a human subject from whom a malignant tumor has been resected and a method of classifying the grade of a malignant tumor, such as a glial tumor, based on a molecular classification.

ABFR L'invention concerne un procede de diagnostic de la presence de tumeurs malignes, y compris de gliomes, chez l'homme, qui implique la detection de la surexpression de la proteine de sous-unite de laminine α4 ou d'un ARNm specifique de la laminine α4, par comparaison avec le niveau d'expression dans un temoin tissulaire normal. L'invention concerne egalement un procede permettant de prevoir la recurrence d'une tumeur maligne chez un homme ayant subi une resection de tumeur maligne, ainsi qu'un procede de determination de la classe d'une tumeur maligne, telle qu'une tumeur gliale, sur la base d'une classification moleculaire.

L14 ANSWER 4 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2002057457 PCTFULL ED 20020801 EW 200230
TITLE (ENGLISH): 55562 AND 21617, NOVEL HUMAN PROTEINS AND METHODS OF USE THEREOF
TITLE (FRENCH): 55562 ET 21617, NOUVELLES PROTEINES HUMAINES ET LEURS METHODES D'UTILISATION
INVENTOR(S): MEYERS, Rachel, A.; BANDARU, Rajasekhar
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC., for all designates States except US; MEYERS, Rachel, A., for US only; BANDARU, Rajasekhar, for US only
AGENT: COLLAZO, Diana, M.
LANGUAGE OF FILING: English
LANGUAGE OF PUBL.: English
DOCUMENT TYPE: Patent
PATENT INFORMATION:

	NUMBER	KIND	DATE
	WO 2002057457	A2	20020725
DESIGNATED STATES	AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG		
APPLICATION INFO.:	WO 2001-US49416	A	20011218
PRIORITY INFO.:	US 2000-60/256,249		20001218
	US 2000-60/256,405		20001218

ABEN The invention provides isolated nucleic acids molecules, designated 21617 and 55562 nucleic acid molecules, which encode novel dehydrogenase or tetratricopeptide repeat members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing 21617 or 55562 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 21617 or 55562 gene has been introduced or disrupted.

The invention still further provides isolated 21617 or 55562 proteins, fusion proteins, antigenic peptides and anti-21617 or 55562 antibodies. Diagnostics methods utilizing compositions of the invention are also provided.

ABFR La presente invention concerne des molecules d'acides nucleiques isolees, designees sous le nom de molecules d'acides nucleiques 21617 et 55562, codant de nouvelles repetitions de la deshydrogenase ou du tetratrichopeptide. L'invention concerne egalement des molecules d'acides nucleiques antisens, des vecteurs d'expression recombines contenant ces molecules d'acides nucleiques 21617 ou 55562, des cellules hotes dans lesquelles ces vecteurs d'expression ont ete introduits et des animaux transgeniques non humains dans lesquels le gene 21617 ou 55562 a ete introduit ou interrompu. L'invention concerne egalement des proteines 21617 ou 55562 isolees, des proteines hybrides, des peptides antigeniques et des anticorps anti-21617 ou 55562. L'invention concerne egalement des methodes diagnostiques utilisant des compositions de la

présente invention.

L2 ANSWER 11 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2000:49185 SCISEARCH
THE GENUINE ARTICLE: 273BX
TITLE: Cell-type specific expression in the pituitary: physiology and gene therapy
AUTHOR: Castro M G (Reprint); Windeatt S; SmithArica J; Lowenstein P R
CORPORATE SOURCE: UNIV MANCHESTER, SCH MED, MOL MED UNIT, ROOM I-302, OXFORD RD, MANCHESTER M13 9PT, LANCS, ENGLAND (Reprint)
COUNTRY OF AUTHOR: ENGLAND
SOURCE: BIOCHEMICAL SOCIETY TRANSACTIONS, (**DEC 1999**) Vol. 27, Part 6, pp. 858-863.
Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON W1N 3AJ, ENGLAND.
ISSN: 0300-5127.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 49

L2 ANSWER 18 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 1998:946863 SCISEARCH
THE GENUINE ARTICLE: 146TR
TITLE: The cytogenesis and pathogenesis of pituitary adenomas
AUTHOR: Asa S L (Reprint); Ezzat S
CORPORATE SOURCE: MT SINAI HOSP, DEPT PATHOL & LAB MED, 600 UNIV AVE, TORONTO, ON M5G 1X5, CANADA (Reprint); MT SINAI HOSP, DEPT MED, TORONTO, ON M5G 1X5, CANADA; UNIV TORONTO, DEPT LAB MED & PATHOBIOL, TORONTO, ON M5G 1X5, CANADA; UNIV TORONTO, DEPT MED, TORONTO, ON M5G 1X5, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: ENDOCRINE REVIEWS, (**DEC 1998**) Vol. 19, No. 6, pp. 798-827.
Publisher: ENDOCRINE SOC, 4350 EAST WEST HIGHWAY SUITE 500, BETHESDA, MD 20814-4110.
ISSN: 0163-769X.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 361

L2 ANSWER 16 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 1999:271844 SCISEARCH
THE GENUINE ARTICLE: 182EY
TITLE: The pathology of pituitary tumors
AUTHOR: Asa S L (Reprint)
CORPORATE SOURCE: MT SINAI HOSP, DEPT PATHOL & LAB MED, 600 UNIV AVE, TORONTO, ON M5G 1X5, CANADA (Reprint); UNIV TORONTO, DEPT LAB MED & PATHOBIOL, TORONTO, ON, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: ENDOCRINOLOGY AND METABOLISM CLINICS OF NORTH AMERICA, (**MAR 1999**) Vol. 28, No. 1, pp. 13-&.
Publisher: W B SAUNDERS CO, INDEPENDENCE SQUARE WEST CURTIS CENTER, STE 300, PHILADELPHIA, PA 19106-3399.
ISSN: 0889-8529.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 153

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The pathologist plays an important role in the distinction of pituitary adenomas from other tumors and tumor-like lesions of the sellar region, and in the accurate morphologic characterization of pitutiary adenomas. A clinicopathologic classification of pituitary adenomas is based on cell differentiation correlated with clinical evidence of hormone secretion; this classification emphasizes clinically relevant features that can offer guidance for patient management. The application of a rational approach to the immunohistochemical analysis of these lesions can be used to evaluate pathogenetic and prognostic markers and to predict responses to specific therapeutic modalities.